

Tue Aug 5 15:09:04 2003

genalign.rec

Winkler, U.
09/303040 v. Page 1
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| 10 | Genetics
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GENALIGN - Multiple Sequence Alignment Program
Release 5.4

Tue 5 Aug 103 15:03:53-PDT

Solution Parameters:

Nucleic Alphabet = Identity
Output Line Length = 80
Compass = Off
Histogram = Off
Randomization = Off
AMINO-Res-Length = 2
Distortion-weight = 5.00
Length-factor = 0
Matching-weight = 1.00
NUCLEIC-Res-Length = 4
Spread-factor = 50

Clustered order of selected sequences:

1. US-09-303-040-5 (1-1080)
80. US-09-303-510-5 (1-1080)

Region Alignment: (listed in clustered order)

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US-09-303- 1 GTTCTGTGTTCTCTGGGAAATGCACTAGAGCTTAAACATCTGTCTCTGGAGCTGCAAGT
US-09-303- 1 GTTCTGTGTTCTCTGGGAAATGCACTAGAGCTTAAACATCTGTCTCTGGAGCTGCAAGT
consensus GTTCTGTGTTCTCTGGGAAATGCACTAGAGCTTAAACATCTGTCTCTGGAGCTGCAAGT

US-09-303- 62 GATGGGCAATTTGACAGACATATGGAAGTCACTGCTCTGTGATAGGAGCTGCTG
US-09-303- 62 GATGGGCAATTTGACAGACATATGGAAGTCACTGCTCTGTGATAGGAGCTGCTG
consensus GATGGGCAATTTGACAGACATATGGAAGTCACTGCTCTGTGATAGGAGCTGCTG

US-09-303- 123 CTCTGTGTGTTCTCTGCAATGAAAGTCAAGCAATTTTCAACAAAGCTGAAAGCTGCAAT
US-09-303- 123 CTCTGTGTGTTCTCTGCAATGAAAGTCAAGCAATTTTCAACAAAGCTGAAAGCTGCAAT
consensus CTCTGTGTGTTCTCTGCAATGAAAGTCAAGCAATTTTCAACAAAGCTGAAAGCTGCAAT

US-09-303- 184 GCCATTTTACAAAGCTCTCAAAACATATAGAGCTGAGAGCTGATATTTTGGAGAGCA
US-09-303- 184 GCCATTTTACAAAGCTCTCAAAACATATAGAGCTGAGAGCTGATATTTTGGAGAGCA
consensus GCCATTTTACAAAGCTCTCAAAACATATAGAGCTGAGAGCTGATATTTTGGAGAGCA

US-09-303- 245 GGAATAGCTGTTCTGTATGAGATATTCAGAGGCAAAAGAAAGCTCAAAATTTTCAATC
US-09-303- 245 GGAATAGCTGTTCTGTATGAGATATTCAGAGGCAAAAGAAAGCTCAAAATTTTCAATC
consensus GGAATAGCTGTTCTGTATGAGATATTCAGAGGCAAAAGAAAGCTCAAAATTTTCAATC

US-09-303- 306 AATATTAAGGCGGTTAACAAGCTTGAACAAGGCAAGCTGAGCCCTGAGATCTCAAAATTTT
US-09-303- 306 AATATTAAGGCGGTTAACAAGCTTGAACAAGGCAAGCTGAGCCCTGAGATCTCAAAATTTT
consensus AATATTAAGGCGGTTAACAAGCTTGAACAAGGCAAGCTGAGCCCTGAGATCTCAAAATTTT
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US-09-303- 367 AGATCAAGACAGAGGCAATATATCTGTTTCAATTAATTAAGGCGCAAGAGCTACT
US-09-303- 367 AGATCAAGACAGAGGCAATATATCTGTTTCAATTAATTAAGGCGCAAGAGCTACT
consensus AGATCAAGACAGAGGCAATATATCTGTTTCAATTAATTAAGGCGCAAGAGCTACT

US-09-303- 428 TCCCATGCAACCAATATGATTTGACCTATGAGTGTCTGTAAGTTCAGTCAAGCTGAATTA
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consensus TCCCATGCAACCAATATGATTTGACCTATGAGTGTCTGTAAGTTCAGTCAAGCTGAATTA

US-09-303- 489 ACGTAACTTCTAATAGACAGAAATTTGCAATCAATTAATTTGACCTGCTCAATATAC
US-09-303- 489 ACGTAACTTCTAATAGACAGAAATTTGCAATCAATTAATTTGACCTGCTCAATATAC
consensus ACGTAACTTCTAATAGACAGAAATTTGCAATCAATTAATTTGACCTGCTCAATATAC

US-09-303- 550 AAGGTTACCCAGAACCTAAGAGATATTAATTTGAGTAAACATGAGAAATTCACATTA
US-09-303- 550 AAGGTTACCCAGAACCTAAGAGATATTAATTTGAGTAAACATGAGAAATTCACATTA
consensus AAGGTTACCCAGAACCTAAGAGATATTAATTTGAGTAAACATGAGAAATTCACATTA

US-09-303- 611 GTATGATACCTGATGAGAAATCTCAAAATTAATGACAGACATGATCAAGCTTTCTATC
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consensus GTATGATACCTGATGAGAAATCTCAAAATTAATGACAGACATGATCAAGCTTTCTATC

US-09-303- 672 AGCTTGCTTTTTCAGTCCCTGAGACACATATGAGAGCTTTTGTGCTCCCTGAAGCTG
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consensus AGCTTGCTTTTTCAGTCCCTGAGACACATATGAGAGCTTTTGTGCTCCCTGAAGCTG

US-09-303- 733 AGACATGAGAGATGCTCTCTCCCTACCTTTCATATGATGACAACTTAAGATTAAGA
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consensus AGACATGAGAGATGCTCTCTCCCTACCTTTCATATGATGACAACTTAAGATTAAGA

US-09-303- 794 CCTGAAACAGAGGCACTTCTCTGATATTTGAGGCTGATCTGTAATTTTGTGTTTGT
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consensus CCTGAAACAGAGGCACTTCTCTGATATTTGAGGCTGATCTGTAATTTTGTGTTTGT

US-09-303- 855 GGAATGCTCTCTTAAACATTAAGGAAAGAAAGAAAGAAAGCTGAGCCCTCTCAATG
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consensus GGAATGCTCTCTTAAACATTAAGGAAAGAAAGAAAGAAAGCTGAGCCCTCTCAATG

US-09-303- 916 AATGTGAAACATTAAGGAAAGAAAGAAAGAAAGAAAGCAAGCAAGCAAGCAAGCAATTA
US-09-303- 916 AATGTGAAACATTAAGGAAAGAAAGAAAGAAAGAAAGCAAGCAAGCAAGCAAGCAATTA
consensus AATGTGAAACATTAAGGAAAGAAAGAAAGAAAGAAAGCAAGCAAGCAAGCAAGCAATTA

US-09-303- 977 CCGCTGCTGAGAGATGATTAATGAGGCTGTTTAACTTTTGAAGAGCTGAGG
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US-09-303- 977 CCACGTACCTGAGATCTGATGAGCCGAGTGTATTACATTTTGAAAGACAGCTCAGGG
consensus CCACGTACCTGAGATCTGATGAGCCGAGTGTATTACATTTTGAAAGACAGCTCAGGG

US-09-303- 1038 GACAAAAATCAGTACGAAATATGTGCTTGCGCTGCTGACAT
|||||
US-09-303- 1038 GACAAAAATCAGTACGAAATATGTGCTTGCGCTGCTGACAT
consensus GACAAAAATCAGTACGAAATATGTGCTTGCGCTGCTGACAT

Alignment score = 1080.00

Scoring matrix:

	3	80
3	1080	
80		

US-09-303-040-5 rev

FASTCD8 - Fast Pairwise Comparison of Sequences
Release 5.4

Query sequence being compared: US-09-303-040-5 (1-1080)
 Number of sequences searched: 1
 Number of scores above cutoff: 1

Student	Score
N	1080
U	1020
M	960
B	900
E	840
R	780
O	720
P	660
C	600
S	540

SEARCH STATISTICS

The scores below are sorted by initial score.
Significance is calculated based on initial score.

Sequence Name	Description
1	

Sequence Name	Description	Init.	Opt.	Length	Score	Score	Sig.	Frame
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1. US-09-303-510-5 Sequence 5. Application file 1000 1000

1. US-09-303-040-5 (1-1080)

US-09-303-510-5 Sequence 5, Application US/09303510A

Sequence 5, Application US/09303510A
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Collision, Blien W.
APPLICANT: Hersh, Stephen W.

APPL.

TITLE OF INVENTION:

TITLE OF INVENTION: CTLA-4 Nucleic Acid and Polypeptide

FILE REFERENCE: 549

CURRENT APPLICATION NUMBER: US/09/303,510A
CURRENT FILING DATE: 2009-03-03

EARLIER APPLICATION NUMBER: 1999-04-30

AFRICATION NUMBER: 60/
EARLIER FILING DATE: 1998-05-07

NUMBER OF SBQ ID NOS: 83

SOFTWARE: PatentIn Ver. 2.1

0000 10 NO 5
1-LENGTH: 1000

2000: 2000
 TYPE: DNA

ORGANISM: *Pellaea*

ORGANISM: *Pelina*

Initial Score	=	1080	Optimized Score	=	1080	Significance	=	0.00
Residue Identity	=	100%	Matches	=	1080	Mismatches	=	0
Gaps	=	0	Conservative Substitutions	=	0	Nonconservative Substitutions	=	0

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X 10 20 30 40 50 60 70
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 430

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510 520 530 540 550 560 570
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